



AGCATTGATGACCCAGACTCCACTCTCCCTGCCTGCTCAGTCTTGGAGATCAAGCCTCCATCTCTTCAGATCTAGTCAGAGCATTTGTA
TCGTAACACTACTGGGTCTGAGGTGAGAGGACGGACAGTCCAGAACCTCTAGTTCGGAGGTAGAGAACGCTCTAGATCAGTCTCGTAACAT
S I V M T Q T P L S L P V S L G D Q A S I S C R S S Q S I V
CATACTAATGGAACACCTATTAGATGGTACCTGCAGAACCCAGGCCAGTCTCCAAACCTCTCATCTACAAAGTTTCCAAACCGATT
GTATCATTACCTTTGGATAAATCTTACCATGGACGCTTTGGTCCGGTCAGAGGTTTGGAGGAGTAGATGTTTCAAAGGTTGGCTAAA
D E
H S N G N T Y L E W Y L Q K P G Q S P N L L I Y K V S N R F
CDR1
TCTGGGGTCCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTCACACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTT
AGACCCAGGGTCTGTCCAGTCCACCGTCACCTAGTCCCTGTCTAAAGTGTGAGTTCTAGTCTCACCCTCCGACTCCTAGACCCCTCAA
S G V P D R F S G S G S G T D F T L K I S R V E A E D L G V
TATTACTGCTTTCAAGGTTTCACATGTTCTCCGACGTTCCGGTGGAGGCCACCAAGCTGGAATCAAAACGGGctgatgctgcaccaactgta
ATAATGACGAAAGTTCCAAAGTGTACAAAGGAGGCTGCAAGCCACCTCCGTTGGTTCGACCTTTAGTTTGGCCgactacgacgtggttgacat
Y Y C F Q G S H V P P T F G G G T K L E I K R
CDR3
tccatcttccaccatccagtgaggatccggc
aggtagaagggtggtaggtcactcctaggccg

Figure 1A

Figure 1B

	1	10	20	27 A B C D E	30
REIVk	DIQMTQSPSSLSASVGDRVTITCQASQ				DI IKYLNW
MN3V _k	SIVM	T L P V L QAS S S			SIVHSNGNT E
hMN3V _k	DIQL		S S S S		SIVHSNGNT E

	40	50	60	70
REIVk	YQQT	PGKAPKLLIYEASN	LAGVPSR	FGSGSGTDYFTI
MN3V _k	L K Q S N	K V R F S		D F L K
hMN3V _k	K	K V S N R F S		D F

	80	90	100	108
REIVk	SSLQPED	IATYQCQQYQSLPYTFGQGT	KVQITR	
MN3V _k	RVEA	GV F GSHV P G	LEIKR	
hMN3V _k		F GSHV P G	EIKR	

Figure 4A.

Replacement Sheet

Figure 4B.